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Gly	Gln	Cys	Gly	Gly	Ile	Asn	Tyr	Asn	Gly	Pro	Thr	Cys	Cys	Gln	Ser	203
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Ser	Thr	Ala	Ser	Tyr	Asn	Gly	Asn	Pro	Phe	Ser	Gly	Val	Gln	Leu	Trp	443
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Ser	Phe	Gln	Trp	Leu	Asp	Arg	Asn	Val	Thr	Val	Asp	Thr	Leu	Phe	Ser	587
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Sequence Listing CBH 10377-WO.ST25

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aac aac tac aag cgc tac atc gac cgg atc cgt gag ctc ctt atc cag Asn Asn Tyr Lys Arg Tyr Ile Asp Arg Ile Arg Glu Leu Leu Ile Gln 225 230 235	779
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gtc aag gga act ggc ttc ggt gtg cgc cct act gct aac act ggg cat Val Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ala Asn Thr Gly His 400 405 410 415	1307
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Sequence Listing CBH 10377-WO.ST25

ctt tcc gac gca ctg act ccg gcg cct gag gct ggc caa tgg ttc cag 1451
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 450 455 460

gct tat ttc gaa cag ctg ctc atc aat gcc aac cct ccg ctc 1493
 Ala Tyr Phe Glu Gln Leu Leu Ile Asn Ala Asn Pro Pro Leu
 465 470 475

tgaacggaag cggagatacc ggaaggcggg gagaagagcg gaattcaagt ctgcttatca 1553

aaatccactc accaagtgga ttaaagcggg tttatacatc tgagaaacaa cctgctttaa 1613

actcttcttg tacatatctc acttcgagac gtgcctcttt ctcaggagca ctgtagatac 1673

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<213> Chaetomium thermophilum NP000980

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Ala Ala Pro Leu Leu Glu Glu Arg Gln Ser Cys Ser Ser Val Trp Gly
 20 25 30

Gln Cys Gly Gly Ile Asn Tyr Asn Gly Pro Thr Cys Cys Gln Ser Gly
 35 40 45

Ser Val Cys Thr Tyr Leu Asn Asp Trp Tyr Ser Gln Cys Ile Pro Gly
 50 55 60

Gln Ala Gln Pro Gly Thr Thr Ser Thr Thr Ala Arg Thr Thr Ser Thr
 65 70 75 80

Ser Thr Thr Ser Thr Ser Ser Val Arg Pro Thr Thr Ser Asn Thr Pro
 85 90 95

Val Thr Thr Ala Pro Pro Thr Thr Thr Ile Pro Gly Gly Ala Ser Ser
 100 105 110

Thr Ala Ser Tyr Asn Gly Asn Pro Phe Ser Gly Val Gln Leu Trp Ala
 115 120 125

Asn Thr Tyr Tyr Ser Ser Glu Val His Thr Leu Ala Ile Pro Ser Leu
 130 135 140

Ser Pro Glu Leu Ala Ala Lys Ala Ala Lys Val Ala Glu Val Pro Ser
 145 150 155 160

Phe Gln Trp Leu Asp Arg Asn Val Thr Val Asp Thr Leu Phe Ser Gly
 165 170 175

Sequence Listing CBH 10377-WO.ST25

Thr Leu Ala Glu Ile Arg Ala Ala Asn Gln Arg Gly Ala Asn Pro Pro
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 Tyr Ala Gly Ile Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala
 195 200 205
 Ala Ala Ala Ser Asn Gly Glu Trp Ser Ile Ala Asn Asn Gly Ala Asn
 210 215 220
 Asn Tyr Lys Arg Tyr Ile Asp Arg Ile Arg Glu Leu Leu Ile Gln Tyr
 225 230 235 240
 Ser Asp Ile Arg Thr Ile Leu Val Ile Glu Pro Asp Ser Leu Ala Asn
 245 250 255
 Met Val Thr Asn Met Asn Val Gln Lys Cys Ser Asn Ala Ala Ser Thr
 260 265 270
 Tyr Lys Glu Leu Thr Val Tyr Ala Leu Lys Gln Leu Asn Leu Pro His
 275 280 285
 Val Ala Met Tyr Met Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro
 290 295 300
 Ala Asn Ile Gln Pro Ala Ala Glu Leu Phe Ala Gln Ile Tyr Arg Asp
 305 310 315 320
 Ala Gly Arg Pro Ala Ala Val Arg Gly Leu Ala Thr Asn Val Ala Asn
 325 330 335
 Tyr Asn Ala Trp Ser Ile Ala Ser Pro Pro Ser Tyr Thr Ser Pro Asn
 340 345 350
 Pro Asn Tyr Asp Glu Lys His Tyr Ile Glu Ala Phe Ala Pro Leu Leu
 355 360 365
 Arg Asn Gln Gly Phe Asp Ala Lys Phe Ile Val Asp Thr Gly Arg Asn
 370 375 380
 Gly Lys Gln Pro Thr Gly Gln Leu Glu Trp Gly His Trp Cys Asn Val
 385 390 395 400
 Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ala Asn Thr Gly His Glu
 405 410 415
 Leu Val Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly
 420 425 430
 Thr Ser Ala Asp Thr Ser Ala Ala Arg Tyr Asp Tyr His Cys Gly Leu
 435 440 445

Sequence Listing CBH 10377-WO.ST25

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 <222> (87)..(87)
 <223> n is a, c, g, or t

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 ctgtttgccc gcatctacaa tgatgccggc aagccggctg ccgtccgcgg cctggccact 840
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Sequence Listing CBH 10377-WO.ST25

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 <213> Myceliophthora thermophila
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Leu Ser Thr Thr Pro Pro Pro Val Ser Ser Pro Arg Asp Gln His Ser
 35 40 45

Arg Arg Cys Asp Leu His Gly Glu Leu Leu Trp Gln Pro Leu Leu Gly
 50 55 60

Arg Pro Ala Leu Arg Gln Arg Leu Leu Gln Val Arg Gly Pro Gln Ser
 65 70 75 80

Arg His Ser His Asp Trp Tyr Ser Gly Gly Ser Arg Leu Pro Pro Ser
 85 90 95

Arg Glu Val Pro Ser Phe Gln Trp Leu Asp Thr Glu Arg Ala Leu Ile
 100 105 110

Arg His Pro Asp Gly Pro Asp Ser Val Pro Arg Ser Gly Leu Ser Ile
 115 120 125

Arg His Gly Glu Gln Ser Tyr Pro Tyr Ala Ala Gln Leu Val Val Tyr
 130 135 140

Asp Leu Pro Asp Arg Asp Cys Ala Ala Ala Ala Ser Asn Gly Glu Phe
 145 150 155 160

Ser Ile Ala Asn Gly Gly Ala Ala Asn Tyr Arg Ser Tyr Ile Asp Ala
 165 170 175

Ile Arg Lys His Ile Ile Glu Tyr Ser Asp Ile Arg Ile Ile Leu Val
 180 185 190

Ile Glu Pro Asp Ser Met Ala Asn Met Val Thr Asn Met Asn Val Ala
 195 200 205

Lys Cys Ser Asn Ala Ala Ser Thr Tyr His Glu Leu Thr Val Tyr Ala

Sequence Listing CBH 10377-WO.ST25

210

215

220

Leu Lys Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly
 225 230 235 240

His Ala Gly Trp Leu Gly Trp Pro Ala Asn Ile Gln Pro Ala Ala Glu
 245 250 255

Leu Phe Ala Gly Ile Tyr Asn Asp Ala Gly Lys Pro Ala Ala Val Arg
 260 265 270

Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Ala Trp Ser Ile Ala Ser
 275 280 285

Ala Pro Ser Tyr Thr Ser Ala Asn Pro Asn Tyr Asp Glu Lys His Tyr
 290 295 300

Ile Glu Ala Phe Ser Pro Leu Leu Asn Ser Ala Gly Phe Pro Ala Arg
 305 310 315 320

Phe Ile Val Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Gln
 325 330 335

Gln Trp Gly Asp Trp Cys Asn Val Lys Gly Thr Gly Phe Gly Val Arg
 340 345 350

Pro Thr Ala Asn Thr Gly His Glu Leu Val Asp Ala Phe Val Trp Val
 355 360 365

Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala Ala Arg
 370 375 380

Tyr Asp Tyr His Cys Gly Leu Ser Asp Ala Leu Gln Pro Ala Pro Glu
 385 390 395 400

Ala Gly Gln Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu Thr Asn Ala
 405 410 415

Asn Pro Pro Phe
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 Tyr Ala Ser Val Tyr Ser Asp Ala Gly Ser Pro Ala Ala Leu Arg Gly

Sequence Listing CBH 10377-WO.ST25

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 Leu Ala Thr Asn Val Ala Asn Tyr Asn Ala Trp Thr Ile Asp Thr Cys
 20 25 30

cct tca tac aca cag ggt aac tcc att tgc gac gag aag gac tac atc 144
 Pro Ser Tyr Thr Gln Gly Asn Ser Ile Cys Asp Glu Lys Asp Tyr Ile
 35 40 45

aat gcg ctt gct ccc ctg ctt cgc agc tca ggg ctt acg gac gct cat 192
 Asn Ala Leu Ala Pro Leu Leu Arg Ser Ser Gly Leu Thr Asp Ala His
 50 55 60

ttc atc act gat acc ggc cgc aac ggc aag caa cca aca ggc caa caa 240
 Phe Ile Thr Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Gln
 65 70 75 80

gcc tgg ggc gac tgg tgc aat gtc atc ggc acg ggc ttt ggc gtg cgc 288
 Ala Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Val Arg
 85 90 95

ccg tcc acg aac aca ggt gat tct tta ctt gac gcc ttc gtc tgg gtt 336
 Pro Ser Thr Asn Thr Gly Asp Ser Leu Leu Asp Ala Phe Val Trp Val
 100 105 110

aaa ccc ggt ggc gag agt gac ggg act tct gat act tgt gcg gcg cgg 384
 Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Cys Ala Ala Arg
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 Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu
 130 135

<210> 6

<211> 139

<212> PRT

<213> Acremonium sp.T178-4 NP001132.

<400> 6

Tyr Ala Ser Val Tyr Ser Asp Ala Gly Ser Pro Ala Ala Leu Arg Gly
 1 5 10 15

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 20 25 30

Pro Ser Tyr Thr Gln Gly Asn Ser Ile Cys Asp Glu Lys Asp Tyr Ile
 35 40 45

Asn Ala Leu Ala Pro Leu Leu Arg Ser Ser Gly Leu Thr Asp Ala His
 50 55 60

Phe Ile Thr Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Gln
 65 70 75 80

Ala Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Val Arg
 85 90 95

Pro Ser Thr Asn Thr Gly Asp Ser Leu Leu Asp Ala Phe Val Trp Val
 100 105 110

Sequence Listing CBH 10377-WO.ST25

Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Cys Ala Ala Arg
 115 120 125

Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu
 130 135

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 <213> Melanocarpus sp. AT181-3 NP001133

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 Asp Ala Gly Lys Pro His Ser Val Arg Gly Leu Ala Thr Asn Val Ala
 1 5 10 15
 aac tac aat gcc tgg agc gtc gcc tcg gcc ccg cct tac acc agc ccc 96
 Asn Tyr Asn Ala Trp Ser Val Ala Ser Ala Pro Pro Tyr Thr Ser Pro
 20 25 30
 aac ccc aac tac gat gag aag cac tac att gag gcc ttc agc cct ctc 144
 Asn Pro Asn Tyr Asp Glu Lys His Tyr Ile Glu Ala Phe Ser Pro Leu
 35 40 45
 ctt gag gcc cgc ggc ttc cct gcc cgc ttc atc gtc gac cag ggc cgc 192
 Leu Glu Ala Arg Gly Phe Pro Ala Arg Phe Ile Val Asp Gln Gly Arg
 50 55 60
 agc ggc aag cag ccc acc ggc cag aag gag tgg ggc cac tgg tgc aac 240
 Ser Gly Lys Gln Pro Thr Gly Gln Lys Glu Trp Gly His Trp Cys Asn
 65 70 75 80
 gct atc ggc acc ggc ttc ggc att cgc ccg acc gcc aac acc ggc cac 288
 Ala Ile Gly Thr Gly Phe Gly Ile Arg Pro Thr Ala Asn Thr Gly His
 85 90 95
 aac ctg gtt gat gcc ttc 306
 Asn Leu Val Asp Ala Phe
 100

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 <212> PRT
 <213> Melanocarpus sp. AT181-3 NP001133

<400> 8

Asp Ala Gly Lys Pro His Ser Val Arg Gly Leu Ala Thr Asn Val Ala
 1 5 10 15

Asn Tyr Asn Ala Trp Ser Val Ala Ser Ala Pro Pro Tyr Thr Ser Pro
 20 25 30

Asn Pro Asn Tyr Asp Glu Lys His Tyr Ile Glu Ala Phe Ser Pro Leu
 35 40 45

Sequence Listing CBH 10377-WO.ST25

Leu Glu Ala Arg Gly Phe Pro Ala Arg Phe Ile Val Asp Gln Gly Arg
 50 55 60

Ser Gly Lys Gln Pro Thr Gly Gln Lys Glu Trp Gly His Trp Cys Asn
 65 70 75 80

Ala Ile Gly Thr Gly Phe Gly Ile Arg Pro Thr Ala Asn Thr Gly His
 85 90 95

Asn Leu Val Asp Ala Phe
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<210> 9
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 <212> DNA
 <213> Thielavia cf. microspora T046-1 NP001134

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 <222> (1)..(432)

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 Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala Gly Ile Tyr Ser Asp
 1 5 10 15
 gct ggc aag ccc gcc tcg gtc cgc ggt ttg gcc acc aac gtg gcc aac 96
 Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala Thr Asn Val Ala Asn
 20 25 30
 tac aac gcc tgg agc ctg tcg tcg gcg ccg tcg tac acg agc ccc aac 144
 Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser Tyr Thr Ser Pro Asn
 35 40 45
 gcc aac tac gac gag aag cac tac gtc gag gcc ttt gcc ccg ctc ctc 192
 Ala Asn Tyr Asp Glu Lys His Tyr Val Glu Ala Phe Ala Pro Leu Leu
 50 55 60
 cag gcg gcc ggc ttc ccc gcc aag ttc atc acc gac acg ggc cgc aac 240
 Gln Ala Ala Gly Phe Pro Ala Lys Phe Ile Thr Asp Thr Gly Arg Asn
 65 70 75 80
 ggc aag cag ccc acg ggc cag agc gcg tgg ggc gac tgg tgc aac gtc 288
 Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val
 85 90 95
 aag ggc acc ggc ttc ggt gtc cgc ccg acc tcg gag acg ggc cac gac 336
 Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ser Glu Thr Gly His Asp
 100 105 110
 ctc ctc gac gcc ttc gtc tgg gtc aag ccc ggt ggc gag tcg gac ggc 384
 Leu Leu Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly
 115 120 125
 acc agc gac acc agc gcc gcc cgc tac gac tac cac tgc ggt ctg tcg 432
 Thr Ser Asp Thr Ser Ala Ala Arg Tyr Asp Tyr His Cys Gly Leu Ser
 130 135 140

<210> 10
 <211> 144
 <212> PRT

Sequence Listing CBH 10377-WO.ST25

<213> Thielavia cf. microspora T046-1 NP001134

<400> 10

Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala Gly Ile Tyr Ser Asp
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Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala Thr Asn Val Ala Asn
20 25 30

Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser Tyr Thr Ser Pro Asn
35 40 45

Ala Asn Tyr Asp Glu Lys His Tyr Val Glu Ala Phe Ala Pro Leu Leu
50 55 60

Gln Ala Ala Gly Phe Pro Ala Lys Phe Ile Thr Asp Thr Gly Arg Asn
65 70 75 80

Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val
85 90 95

Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ser Glu Thr Gly His Asp
100 105 110

Leu Leu Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly
115 120 125

Thr Ser Asp Thr Ser Ala Ala Arg Tyr Asp Tyr His Cys Gly Leu Ser
130 135 140

<210> 11

<211> 297

<212> DNA

<213> Aspergillus sp. T186-2 NP001136

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<222> (1)..(297)

<400> 11

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Gly Leu Phe Gly Trp Pro Ala Asn Leu Thr Pro Ser Ala Arg Leu Phe
1 5 10 15

gcc caa atc tac aag gat gcc ggc agg tct gcc ttc atc cgt ggt ctt 96
Ala Gln Ile Tyr Lys Asp Ala Gly Arg Ser Ala Phe Ile Arg Gly Leu
20 25 30

gcc acc aac gtc tcc aac tac aac gcc ctc agt gca acc acc cgt gat 144
Ala Thr Asn Val Ser Asn Tyr Asn Ala Leu Ser Ala Thr Thr Arg Asp
35 40 45

ccc gtc acc cag ggc aat gac aac tac gat gag ctc cgc ttc atc aac 192
Pro Val Thr Gln Gly Asn Asp Asn Tyr Asp Glu Leu Arg Phe Ile Asn
50 55 60

gct ctt gct cct ctc ctc cga aat gaa ggc tgg gac gcc aag ttc atc 240

Sequence Listing CBH 10377-WO.ST25

Ala Leu Ala Pro Leu Leu Arg Asn Glu Gly Trp Asp Ala Lys Phe Ile
65 70 75 80

gtc gac cag ggt cgt tct ggt gtc cag aac atc cga cag gag tgg ggc 288
Val Asp Gln Gly Arg Ser Gly Val Gln Asn Ile Arg Gln Glu Trp Gly 95

gac tgg tgc 297
Asp Trp Cys

<210> 12
<211> 99
<212> PRT
<213> *Aspergillus* sp. T186-2 NP001136
<400> 12

Gly Leu Phe Gly Trp Pro Ala Asn Leu Thr Pro Ser Ala Arg Leu Phe
1 5 10 15

Ala Gln Ile Tyr Lys Asp Ala Gly Arg Ser Ala Phe Ile Arg Gly Leu
20 25 30

Ala Thr Asn Val Ser Asn Tyr Asn Ala Leu Ser Ala Thr Thr Arg Asp
35 40 45

Pro Val Thr Gln Gly Asn Asp Asn Tyr Asp Glu Leu Arg Phe Ile Asn
50 55 60

Ala Leu Ala Pro Leu Leu Arg Asn Glu Gly Trp Asp Ala Lys Phe Ile
65 70 75 80

Val Asp Gln Gly Arg Ser Gly Val Gln Asn Ile Arg Gln Glu Trp Gly
85 90 95

Asp Trp Cys

<210> 13
<211> 420
<212> DNA
<213> *Thielavia* cf. *australiensis* T55-15 NP001000

<220>
<221> CDS
<222> (1)..(420)

<400> 13 48
tgg ctg ggg tgg ccc gcc aac atc cag ccc gct gct acc ctg ttc gcc
Trp Leu Gly Trp Pro Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala
1 5 10 15

ggc atc tac aac gac gct ggc aag ccc gcc tcg gtc cgt ggt ctg gcc 96
Gly Ile Tyr Asn Asp Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala
20 25 30

acc aac gtt gcc aac tac aac gcc tgg agc ctg tcc tcg gcc ccg tcg 144
Thr Asn Val Ala Asn Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser

Sequence Listing CBH 10377-WO.ST25

35	40	45	
tac acg acc ccc aac gcc aac tac gac gag aag cac tac gtc gag gcc			192
Tyr Thr Thr Pro Asn Ala Asn Tyr Asp Glu Lys His Tyr Val Glu Ala			
50	55	60	
ttt gcc ccg ctt ctc tcg gcc gct ggc ttc ccc gcc aag ttc atc acc			240
Phe Ala Pro Leu Leu Ser Ala Ala Gly Phe Pro Ala Lys Phe Ile Thr			
65	70	75	80
gac act ggc cgc aac ggc aag cag ccc acc ggc cag agc cag tgg ggc			288
Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Ser Gln Trp Gly			
	85	90	95
gat tgg tgc aac gtc aag ggc acc ggc ttc ggt gtc cgc ccg acc tcc			336
Asp Trp Cys Asn Val Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ser			
	100	105	110
gag acg ggc cac gag ctc ctg gat gcc ttt gtc tgg gcc aag ccc ggt			384
Glu Thr Gly His Glu Leu Leu Asp Ala Phe Val Trp Ala Lys Pro Gly			
	115	120	125
ggc gag tcc gac ggt acc agc gac acc agc gct gcc			420
Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala Ala			
	130	135	140

<210> 14

<211> 140

<212> PRT

<213> Thielavia cf. australiensis T55-15 NP001000

<400> 14

Trp Leu Gly Trp Pro Ala Asn Ile Gln Pro Ala Ala Thr Leu Phe Ala
1 5 10 15

Gly Ile Tyr Asn Asp Ala Gly Lys Pro Ala Ser Val Arg Gly Leu Ala
20 25 30

Thr Asn Val Ala Asn Tyr Asn Ala Trp Ser Leu Ser Ser Ala Pro Ser
35 40 45

Tyr Thr Thr Pro Asn Ala Asn Tyr Asp Glu Lys His Tyr Val Glu Ala
50 55 60

Phe Ala Pro Leu Leu Ser Ala Ala Gly Phe Pro Ala Lys Phe Ile Thr
65 70 75 80

Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr Gly Gln Ser Gln Trp Gly
85 90 95

Asp Trp Cys Asn Val Lys Gly Thr Gly Phe Gly Val Arg Pro Thr Ser
100 105 110

Glu Thr Gly His Glu Leu Leu Asp Ala Phe Val Trp Ala Lys Pro Gly
115 120 125

Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala Ala
130 135 140

Sequence Listing CBH 10377-WO.ST25

<210> 15
 <211> 1221
 <212> DNA
 <213> *Aspergillus tubingensis* NP001143

<220>
 <221> CDS
 <222> (1)..(1221)

<220>
 <221> misc_feature
 <222> (903)..(903)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (1011)..(1011)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (1017)..(1017)
 <223> n is a, c, g, or t

<400> 15
 atg aat atg cac tcc atc aac atg cga gcc atc tgg ccc ctc gtc tct 48
 Met Asn Met His Ser Ile Asn Met Arg Ala Ile Trp Pro Leu Val Ser
 1 5 10 15
 ctc ttc tct gcc gtt aag gcc ctc ccc gcc gca agc gcg act gct tca 96
 Leu Phe Ser Ala Val Lys Ala Leu Pro Ala Ala Ser Ala Thr Ala Ser
 20 25 30
 gcg tct gtt gcg gcc tcg agc tct ccg gcg ccg act gcc tct gct acc 144
 Ala Ser Val Ala Ala Ser Ser Ser Pro Ala Pro Thr Ala Ser Ala Thr
 35 40 45
 ggc aat ccc ttt gag gga tac cag ctc tat gtg aac ccc tac tat aag 192
 Gly Asn Pro Phe Glu Gly Tyr Gln Leu Tyr Val Asn Pro Tyr Tyr Lys
 50 55 60
 tcg caa gtg gag agt tcg gcc att cca tca ttg tct gct agt tcg ctg 240
 Ser Gln Val Glu Ser Ser Ala Ile Pro Ser Leu Ser Ala Ser Ser Leu
 65 70 75 80
 gtc gcg cag gcg agt gct gca gcc gat gtg cct tca ttt tac tgg cta 288
 Val Ala Gln Ala Ser Ala Ala Ala Asp Val Pro Ser Phe Tyr Trp Leu
 85 90 95
 gac acg gcc gac aag gtg cct acc atg ggt gaa tat ctg gat gac atc 336
 Asp Thr Ala Asp Lys Val Pro Thr Met Gly Glu Tyr Leu Asp Asp Ile
 100 105 110
 cag acg caa aac gcc gct gga gcg aat cct ccc att gct ggt atc ttc 384
 Gln Thr Gln Asn Ala Ala Gly Ala Asn Pro Pro Ile Ala Gly Ile Phe
 115 120 125
 gtc gtc tat gac ctg ccg gat cgg gat tgc gct gcc ttg gct agt aat 432
 Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn
 130 135 140
 ggg gaa tac gcg atc agt gat gga ggc gtg gag aag tat aag gcg tac 480
 Gly Glu Tyr Ala Ile Ser Asp Gly Gly Val Glu Lys Tyr Lys Ala Tyr
 145 150 155 160

Sequence Listing CBH 10377-WO.ST25

att gat tct att cgc gag cag gtc gag acg tac tcg gat gtt cag act	528
Ile Asp Ser Ile Arg Glu Gln Val Glu Thr Tyr Ser Asp Val Gln Thr	
165 170 175	
att ttg att atc gaa ccg gat agc tta gct aac ctg gtg acg aat ctc	576
Ile Leu Ile Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu	
180 185 190	
gat gtg gct aaa tgc gcc aat gct caa tct gct tac ctg gaa tgc acc	624
Asp Val Ala Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Thr	
195 200 205	
aat tat gca ctt gag cag ttg aat ctr ccg aac gtg gct atg tat ctt	672
Asn Tyr Ala Leu Glu Gln Leu Asn Xaa Pro Asn Val Ala Met Tyr Leu	
210 215 220	
gat gct ggc cat gct gga tgg ctg gga tgg cct gcc aac atc ggt ccc	720
Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Ile Gly Pro	
225 230 235 240	
gcg gcg gaa ctc tac gca tcg gtg tat aag aat gcg tcg tct cca gca	768
Ala Ala Glu Leu Tyr Ala Ser Val Tyr Lys Asn Ala Ser Ser Pro Ala	
245 250 255	
gct gtt cgt gga ctc gct aca rac gta gct aac ttc aat gcc tgg agc	816
Ala Val Arg Gly Leu Ala Thr Xaa Val Ala Asn Phe Asn Ala Trp Ser	
260 265 270	
atc gac act tgc ccc tcc tat acw tcg ggt aac gat gtc tgt gat gaa	864
Ile Asp Thr Cys Pro Ser Tyr Xaa Ser Gly Asn Asp Val Cys Asp Glu	
275 280 285	
aaa agc tac atc aat gcc ttt gca ccg gag ctc tct agn gct gga ttt	912
Lys Ser Tyr Ile Asn Ala Phe Ala Pro Glu Leu Ser Xaa Ala Gly Phe	
290 295 300	
gat gcc cac ttt att acc gat acg ggt cgc aat gga aag cag cct act	960
Asp Ala His Phe Ile Thr Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr	
305 310 315 320	
gga caa agc gcg tgg ggt gac tgg ggc aat gtc aag gat act ggc ttc	1008
Gly Gln Ser Ala Trp Gly Asp Trp Gly Asn Val Lys Asp Thr Gly Phe	
325 330 335	
ggn gct can ccg aca acc gat act gga aac gag ctg gct gat gcc ttt	1056
Gly Ala Xaa Pro Thr Thr Asp Thr Gly Asn Glu Leu Ala Asp Ala Phe	
340 345 350	
gtc tgg gyc aac cct ggc gga aag agt gat ggg acg tcg gac act agc	1104
Val Trp Xaa Asn Pro Gly Gly Lys Ser Asp Gly Thr Ser Asp Thr Ser	
355 360 365	
tct tct cgc tac gat gcg cat tgc gga tat agt gat gct ttg cag cct	1152
Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu Gln Pro	
370 375 380	
gcc ccg gag gct ggt act tgg ttc cag gca tac ttt gag cag ctt ttg	1200
Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu	
385 390 395 400	
acc aat gcc aac cct tcc ctg	1221
Thr Asn Ala Asn Pro Ser Leu	
405	

<210> 16
 <211> 407
 <212> PRT

Sequence Listing CBH 10377-WO.ST25

<213> Aspergillus tubingensis NP001143

<220>

<221> misc_feature

<222> (217)..(217)

<223> The 'Xaa' at location 217 stands for Leu.

<220>

<221> misc_feature

<222> (264)..(264)

<223> The 'Xaa' at location 264 stands for Asp, or Asn.

<220>

<221> misc_feature

<222> (280)..(280)

<223> The 'Xaa' at location 280 stands for Thr.

<220>

<221> misc_feature

<222> (301)..(301)

<223> The 'Xaa' at location 301 stands for Arg, or Ser.

<220>

<221> misc_feature

<222> (339)..(339)

<223> The 'Xaa' at location 339 stands for Gln, or His.

<220>

<221> misc_feature

<222> (355)..(355)

<223> The 'Xaa' at location 355 stands for Ala, or Val.

<400> 16

Met	Asn	Met	His	Ser	Ile	Asn	Met	Arg	Ala	Ile	Trp	Pro	Leu	Val	Ser
1				5					10					15	

Leu	Phe	Ser	Ala	Val	Lys	Ala	Leu	Pro	Ala	Ala	Ser	Ala	Thr	Ala	Ser
			20				25						30		

Ala	Ser	Val	Ala	Ala	Ser	Ser	Ser	Pro	Ala	Pro	Thr	Ala	Ser	Ala	Thr
		35					40					45			

Gly	Asn	Pro	Phe	Glu	Gly	Tyr	Gln	Leu	Tyr	Val	Asn	Pro	Tyr	Tyr	Lys
	50					55					60				

Ser	Gln	Val	Glu	Ser	Ser	Ala	Ile	Pro	Ser	Leu	Ser	Ala	Ser	Ser	Leu
65					70					75					80

Val	Ala	Gln	Ala	Ser	Ala	Ala	Ala	Asp	Val	Pro	Ser	Phe	Tyr	Trp	Leu
				85					90					95	

Asp	Thr	Ala	Asp	Lys	Val	Pro	Thr	Met	Gly	Glu	Tyr	Leu	Asp	Asp	Ile
			100					105					110		

Gln	Thr	Gln	Asn	Ala	Ala	Gly	Ala	Asn	Pro	Pro	Ile	Ala	Gly	Ile	Phe
		115					120					125			

Val	Val	Tyr	Asp	Leu	Pro	Asp	Arg	Asp	Cys	Ala	Ala	Leu	Ala	Ser	Asn
	130					135					140				

Sequence Listing CBH 10377-WO.ST25

Gly Glu Tyr Ala Ile Ser Asp Gly Gly Val Glu Lys Tyr Lys Ala Tyr
 145 150 155 160
 Ile Asp Ser Ile Arg Glu Gln Val Glu Thr Tyr Ser Asp Val Gln Thr
 165 170 175
 Ile Leu Ile Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu
 180 185 190
 Asp Val Ala Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Thr
 195 200 205
 Asn Tyr Ala Leu Glu Gln Leu Asn Xaa Pro Asn Val Ala Met Tyr Leu
 210 215 220
 Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Ile Gly Pro
 225 230 235 240
 Ala Ala Glu Leu Tyr Ala Ser Val Tyr Lys Asn Ala Ser Ser Pro Ala
 245 250 255
 Ala Val Arg Gly Leu Ala Thr Xaa Val Ala Asn Phe Asn Ala Trp Ser
 260 265 270
 Ile Asp Thr Cys Pro Ser Tyr Xaa Ser Gly Asn Asp Val Cys Asp Glu
 275 280 285
 Lys Ser Tyr Ile Asn Ala Phe Ala Pro Glu Leu Ser Xaa Ala Gly Phe
 290 295 300
 Asp Ala His Phe Ile Thr Asp Thr Gly Arg Asn Gly Lys Gln Pro Thr
 305 310 315 320
 Gly Gln Ser Ala Trp Gly Asp Trp Gly Asn Val Lys Asp Thr Gly Phe
 325 330 335
 Gly Ala Xaa Pro Thr Thr Asp Thr Gly Asn Glu Leu Ala Asp Ala Phe
 340 345 350
 Val Trp Xaa Asn Pro Gly Gly Lys Ser Asp Gly Thr Ser Asp Thr Ser
 355 360 365
 Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser Asp Ala Leu Gln Pro
 370 375 380
 Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu
 385 390 395 400
 Thr Asn Ala Asn Pro Ser Leu
 405

Sequence Listing CBH 10377-WO.ST25

<210> 17
 <211> 429
 <212> DNA
 <213> Gloeophyllum trabeum NP001144

<220>
 <221> CDS
 <222> (1)..(429)

<400> 17
 gca tcg tct cca gca gct gtt cgt gga ctc gct aca aac gta gct aac 48
 Ala Ser Ser Pro Ala Ala Val Arg Gly Leu Ala Thr Asn Val Ala Asn
 1 5 10 15
 ttc aat gcc tgg agc atc gac act tgc ccc tcc tat aca tcg ggt aac 96
 Phe Asn Ala Trp Ser Ile Asp Thr Cys Pro Ser Tyr Thr Ser Gly Asn
 20 25 30
 gat gtc tgt gat gag aag agc tac atc aat gcc ttt gca ccg gag ctc 144
 Asp Val Cys Asp Glu Lys Ser Tyr Ile Asn Ala Phe Ala Pro Glu Leu
 35 40 45
 tct agt gct gga ttt gat gcc cac ttt att acc gat acg ggt cgc aat 192
 Ser Ser Ala Gly Phe Asp Ala His Phe Ile Thr Asp Thr Gly Arg Asn
 50 55 60
 gga aag cag cct act gga cag agc gcg tgg ggt gac tgg tgc aat gtc 240
 Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val
 65 70 75 80
 aag gat act ggc ttc ggt gct cag ccg acg acc gat act gga gac gag 288
 Lys Asp Thr Gly Phe Gly Ala Gln Pro Thr Thr Asp Thr Gly Asp Glu
 85 90 95
 ctg gct gat gcc ttt gtc tgg gtc aag cct ggc gga gag agt gat ggg 336
 Leu Ala Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly
 100 105 110
 acg tcg gac act agc tct tct cgc tac gat gcg cat tgc gga tat agt 384
 Thr Ser Asp Thr Ser Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser
 115 120 125
 gat gct ttg cag cct gcc ccg gag gct ggt act tgg ttc caa ggc 429
 Asp Ala Leu Gln Pro Ala Pro Glu Ala Gly Thr Trp Phe Gln Gly
 130 135 140

<210> 18
 <211> 143
 <212> PRT
 <213> Gloeophyllum trabeum NP001144

<400> 18
 Ala Ser Ser Pro Ala Ala Val Arg Gly Leu Ala Thr Asn Val Ala Asn
 1 5 10 15
 Phe Asn Ala Trp Ser Ile Asp Thr Cys Pro Ser Tyr Thr Ser Gly Asn
 20 25 30
 Asp Val Cys Asp Glu Lys Ser Tyr Ile Asn Ala Phe Ala Pro Glu Leu
 35 40 45

Sequence Listing CBH 10377-WO.ST25

Ser Ser Ala Gly Phe Asp Ala His Phe Ile Thr Asp Thr Gly Arg Asn
 50 55 60

Gly Lys Gln Pro Thr Gly Gln Ser Ala Trp Gly Asp Trp Cys Asn Val
 65 70 75 80

Lys Asp Thr Gly Phe Gly Ala Gln Pro Thr Thr Asp Thr Gly Asp Glu
 85 90 95

Leu Ala Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly
 100 105 110

Thr Ser Asp Thr Ser Ser Ser Arg Tyr Asp Ala His Cys Gly Tyr Ser
 115 120 125

Asp Ala Leu Gln Pro Ala Pro Glu Ala Gly Thr Trp Phe Gln Gly
 130 135 140

<210> 19
 <211> 213
 <212> DNA
 <213> Meripilus giganteus ND001631

<220>
 <221> misc_feature
 <222> (1)..(213)
 <223> y is c o r t

<400> 19
 aaactcggag tacgtctgga acaagtgccg gcctcnggcr gctgggtacc gtcttcgtcc 60
 gacagacagc asgtgctgtc gtaccggttg cgacgagctg ttcgaggtay cgtcggactc 120
 ryctccgggm ttcacccaga tkatcacgtc tatgasyggg ttgcccggtg tcgtcctcat 180
 ggcgcgtgcc gaagccgttg cccttgatgt tgc 213

<210> 20
 <211> 71
 <212> PRT
 <213> Meripilus giganteus ND001631 enzyme

<220>
 <221> MISC_FEATURE
 <222> (1)..(71)
 <223> x is any amino acid

<400> 20

Ala Thr Ser Arg Ala Thr Ala Ser Ala Arg Ala Met Arg Thr Asn Thr
 1 5 10 15

Gly Asn Pro Xaa Ile Asp Val Ile Ile Trp Val Xaa Pro Gly Xaa Glu
 20 25 30

Ser Asp Xaa Thr Ser Asn Ser Ser Ser Xaa Pro Val Arg Gln His Xaa

Sequence Listing CBH 10377-WO.ST25

35

40

45

Leu Ser Val Gly Arg Arg Arg Tyr Pro Ala Ala Xaa Gly Arg His Leu
 50 55 60

Phe Gln Thr Tyr Ser Glu Phe
 65 70

<210> 21
 <211> 782
 <212> DNA
 <213> Trichophaea saccata NP000960

<220>
 <221> CDS
 <222> (43)..(702)

<400> 21
 ggcacgaggg cagatcgatc gactcgagga ccacatcgca tc atg aag aac ttc 54
 Met Lys Asn Phe
 1

ctt ctg gcg tcc gcg ctg atc gcg gtt gcc gca gct cag cag agt gct 102
 Leu Leu Ala Ser Ala Leu Ile Ala Val Ala Ala Gln Gln Ser Ala
 5 10 15 20

tgg gga cag tgc ggt gga att ggc tgg act ggc gcg acg act tgt atc 150
 Trp Gly Gln Cys Gly Gly Ile Gly Trp Thr Gly Ala Thr Thr Cys Ile
 25 30 35

tct ggc tac acg tgc tca aag atc aac gac tac tat tcc cag tgc att 198
 Ser Gly Tyr Thr Cys Ser Lys Ile Asn Asp Tyr Tyr Ser Gln Cys Ile
 40 45 50

ccg ggt acg gct tca acc acc act caa ggc ggc ggc aat ggc gga gga 246
 Pro Gly Thr Ala Ser Thr Thr Thr Gln Gly Gly Gly Asn Gly Gly Gly
 55 60 65

aac ggc ggt aca acg act act ccc act acc act cca gcg gcc agt aac 294
 Asn Gly Gly Thr Thr Thr Pro Thr Thr Thr Pro Ala Ala Ser Asn
 70 75 80

acc aac aac ccg ttc tcc ggc aag acc caa tgg gcg aac cct tac tac 342
 Thr Asn Asn Pro Phe Ser Gly Lys Thr Gln Trp Ala Asn Pro Tyr Tyr
 85 90 95 100

gct tcc gag gtc tcg agc atc gcc atc ccg tcc ctc gtt gcc gcc gga 390
 Ala Ser Glu Val Ser Ser Ile Ala Ile Pro Ser Leu Val Ala Ala Gly
 105 110 115

aac acc cac tac atc gtc gac caa ggc cgc agc ggc aag cag ccg acc 438
 Asn Thr His Tyr Ile Val Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr
 120 125 130

ggc cag ctc cag cag ggc gat tgg tgc aac gcc ctg gga acc ggc ttt 486
 Gly Gln Leu Gln Gln Gly Asp Trp Cys Asn Ala Leu Gly Thr Gly Phe
 135 140 145

gga att cgt cct gat aca acc ccg gat gat ccc aac ctt gat gct ttc 534
 Gly Ile Arg Pro Asp Thr Thr Pro Asp Asp Pro Asn Leu Asp Ala Phe
 150 155 160

gtg tgg gtt aag ccg ggt ggt gaa tcg gat ggt acc agc aat act tcc 582
 Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asn Thr Ser

Sequence Listing CBH 10377-WO.ST25

165		170	175	180	
tcg acc cgc tat gat tat cat tgt gga cag agc gat gcg cta caa ccg					630
Ser Thr Arg Tyr Asp Tyr His Cys Gly Gln Ser Asp Ala Leu Gln Pro		185	190	195	
gcc ccg gag gcg gga acg tgg ttc cag gcg tat ttt gtg cag ttg ctg					678
Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu		200	205	210	
cag aat gct aat cct agc ttc acg taagcttggg agcgtggggg ttggaagatg					732
Gln Asn Ala Asn Pro Ser Phe Thr		215	220		
tgtattgtat gtgtagatag agaaaaactg ttggcctatt caggactaag					782

<210> 22
 <211> 220
 <212> PRT
 <213> Trichophaea saccata NP000960

<400> 22

Met Lys Asn Phe Leu Leu Ala Ser Ala Leu Ile Ala Val Ala Ala Ala
 1 5 10 15

Gln Gln Ser Ala Trp Gly Gln Cys Gly Gly Ile Gly Trp Thr Gly Ala
 20 25 30

Thr Thr Cys Ile Ser Gly Tyr Thr Cys Ser Lys Ile Asn Asp Tyr Tyr
 35 40 45

Ser Gln Cys Ile Pro Gly Thr Ala Ser Thr Thr Thr Gln Gly Gly Gly
 50 55 60

Asn Gly Gly Gly Asn Gly Gly Thr Thr Thr Thr Pro Thr Thr Thr Pro
 65 70 75 80

Ala Ala Ser Asn Thr Asn Asn Pro Phe Ser Gly Lys Thr Gln Trp Ala
 85 90 95

Asn Pro Tyr Tyr Ala Ser Glu Val Ser Ser Ile Ala Ile Pro Ser Leu
 100 105 110

Val Ala Ala Gly Asn Thr His Tyr Ile Val Asp Gln Gly Arg Ser Gly
 115 120 125

Lys Gln Pro Thr Gly Gln Leu Gln Gln Gly Asp Trp Cys Asn Ala Leu
 130 135 140

Gly Thr Gly Phe Gly Ile Arg Pro Asp Thr Thr Pro Asp Asp Pro Asn
 145 150 155 160

Leu Asp Ala Phe Val Trp Val Lys Pro Gly Gly Glu Ser Asp Gly Thr
 165 170 175

Sequence EVS181g Cbl 10577-1058125
Ser Asn Thr Ser Thr Arg Tyr Asp Tyr His Cys Gly Gln Ser Asp
180 185 190

Ala Leu Gln Pro Ala Pro Glu Ala Gly Thr Trp Phe Gln Ala Tyr Phe
195 200 205

Val Gln Leu Leu Gln Asn Ala Asn Pro Ser Phe Thr
210 215 220

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<210> 23
<211> 1587
<212> DNA
<213> Stibella annulata NP001040
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<220>
<221> CDS
<222> (21) .. (1394)

<400>	23															53		
ggc	cac	gag	ggc	gcg	cat	caca	atg	gcc	ggt	cga	ttc	ttc	ctc	tct	gct	gcc	ttc	
							Met	Ala	Gly	Arg	Phe	Phe	Leu	Ser	Ala	Ala	Phe	
							1				5					10		
ctg	gct	agc	gcg	gct	tgt	gcc	gtc	cct	ctc	gag	gag	agg	cag	aac	tgc			101
Leu	Ala	Ser	Ala	Ala	Leu	Ala	Val	Pro	Leu	Glu	Glu	Arg	Gln	Asn	Cys			
			15					20					25					
tcc	ccg	cag	tgg	gcc	cag	tgc	ggt	gga	aat	gga	tgg	agc	ggt	ccg	acg			149
Ser	Pro	Gln	Trp	Ala	Gln	Cys	Gly	Gly	Asn	Gly	Trp	Ser	Gly	Pro	Thr			
		30					35					40						
tgc	tgc	gcc	tcc	ggc	agc	aac	tgc	cag	gtc	acc	aac	gag	tgg	tac	tct			197
Cys	Cys	Ala	Ser	Gly	Ser	Asn	Cys	Gln	Val	Thr	Asn	Glu	Trp	Tyr	Ser			
	45					50					55							
cag	tgt	gtt	ccg	ggc	gcg	gcc	cct	ccc	cct	ccc	ccc	gtc	acc	acg	acg			245
Gln	Cys	Val	Pro	Gly	Ala	Ala	Pro	Pro	Pro	Pro	Pro	Val	Thr	Thr	Thr			
					65					70					75			
cgg	tcg	acc	acc	acg	ccc	ccg	acg	acg	acg	acc	agg	acc	acc	gct	gat			293
Arg	Ser	Thr	Thr	Thr	Pro	Pro	Thr	Thr	Thr	Thr	Arg	Thr	Thr	Ala	Asp			
				80						85				90				
gcc	cct	cct	ccc	acc	ggc	ggc	gct	act	tac	acc	ggc	aac	ccc	ttc	ctc			341
Ala	Pro	Pro	Pro	Thr	Gly	Gly	Ala	Thr	Tyr	Thr	Gly	Asn	Pro	Phe	Leu			
			95					100					105					
ggt	gtc	aac	cag	tgg	gcc	aac	aac	ttc	tac	cgg	tct	gag	atc	atg	aac			389
Gly	Val	Asn	Gln	Trp	Ala	Asn	Asn	Phe	Tyr	Arg	Ser	Glu	Ile	Met	Asn			
		110				115						120						
atc	gcc	gtc	ccg	tcc	ctg	tcc	ggt	gcc	atg	gct	acc	gcc	gcc	gcc	aag			437
Ile	Ala	Val	Pro	Ser	Leu	Ser	Gly	Ala	Met	Ala	Thr	Ala	Ala	Ala	Lys			
	125					130					135							
gtc	gcc	gat	gtg	ccc	acc	ttc	cag	tgg	att	gac	aag	atg	gac	aag	ctc			485
Val	Ala	Asp	Val	Pro	Thr	Phe	Gln	Trp	Ile	Asp	Lys	Met	Asp	Lys	Leu			
	140				145					150					155			
ccc	ttg	atc	gat	gag	gct	ctc	gcc	gac	gtc	cgc	gct	gcc	aac	gcc	cgt			533
Pro	Leu	Ile	Asp	Glu	Ala	Leu	Ala	Asp	Val	Arg	Ala	Ala	Asn	Ala	Arg			
				160					165					170				
ggc	ggc	aac	tac	gct	tcc	atc	ctg	gtc	gtc	tac	aac	ctg	ccc	gac	cgt			581

Sequence Listing CBH 10377-WO.ST25																
Gly	Gly	Asn	Tyr 175	Ala	Ser	Ile	Leu	Val 180	Val	Tyr	Asn	Leu	Pro 185	Asp	Arg	
gac Asp	tgc Cys	gcc Ala 190	gcc Ala	gcc Ala	gcc Ala	tcg Ser	aac Asn 195	ggc Gly	gag Glu	ttc Phe	gcc Ala	atc Ile 200	gcc Ala	gac Asp	ggc Gly	629
ggt Gly	gtt Val 205	gct Ala	aag Lys	tac Tyr	aag Lys	aac Asn 210	tac Tyr	att Ile	gac Asp	gag Glu	att Ile 215	cgc Arg	aag Lys	ctc Leu	gtc Val	677
atc Ile 220	aag Lys	tac Tyr	aac Asn	gac Asp	ctc Leu 225	cgt Arg	atc Ile	atc Ile	ctg Leu	gtc Val 230	atc Ile	gag Glu	ccc Pro	gac Asp	tcc Ser 235	725
ctc Leu	gcc Ala	aac Asn	atg Met	gtg Val 240	acc Thr	aac Asn	atg Met	aac Asn	gtc Val 245	gcc Ala	aag Lys	tgc Cys	cag Gln	aac Asn 250	gcc Ala	773
gcc Ala	tcg Ser	gcc Ala	tac Tyr 255	cgg Arg	gag Glu	tgc Cys	acc Thr	aac Asn 260	tat Tyr	gcc Ala	ctg Leu	acg Thr	aac Asn 265	ctc Leu	gac Asp	821
ctg Leu	ccc Pro	aac Asn 270	gtc Val	gcc Ala	cag Gln	tac Tyr	atg Met 275	gat Asp	gcc Ala	gga Gly	cat His	gct Ala 280	ggc Gly	tgg Trp	ctc Leu	869
ggc Gly	tgg Trp 285	ccc Pro	gcc Ala	aac Asn	atc Ile	acc Thr 290	ccc Pro	gcc Ala	gcc Ala	cag Gln	ctc Leu 295	ttc Phe	gcc Ala	gag Glu	gtc Val	917
tac Tyr 300	aag Lys	cag Gln	gcc Ala	ggc Gly	agc Ser 305	ccc Pro	aag Lys	tcg Ser	gtc Val	cgt Arg 310	ggc Gly	ctg Leu	gcc Ala	atc Ile	aac Asn 315	965
gtc Val	tcc Ser	aac Asn	tac Tyr	aac Asn 320	gcg Ala	tgg Trp	agc Ser	gtt Val	tcg Ser 325	tcc Ser	cct Pro	cct Pro	ccc Pro	tac Tyr 330	acc Thr	1013
tct Ser	ccc Pro	aac Asn	ccc Pro 335	aac Asn	tac Tyr	gac Asp	gag Glu	cgc Arg 340	cac His	ttc Phe	gtt Val	gag Glu	gcc Ala 345	ttt Phe	gcg Ala	1061
ccc Pro	ctc Leu	ctg Leu 350	cgc Arg	cag Gln	aac Asn	ggc Gly	tgg Trp 355	gat Asp	gcc Ala	aag Lys	ttc Phe	atc Ile 360	gtc Val	gac Asp	cag Gln	1109
ggc Gly	cgc Arg 365	tcc Ser	ggc Gly	agg Arg	cag Gln	ccc Pro 370	acc Thr	ggc Gly	cag Gln	cag Gln	gag Glu 375	tgg Trp	gga Gly	cac His	tgg Trp	1157
tgc Cys 380	aac Asn	gcc Ala	atc Ile	ggc Gly	act Thr 385	ggc Gly	ttc Phe	ggc Gly	cag Gln	cgc Arg 390	ccg Pro	acg Thr	tcc Ser	aac Asn	acc Thr 395	1205
ggc Gly	cac His	gcc Ala	gat Asp	gtt Val 400	gac Asp	gct Ala	ttc Phe	gtc Val	tgg Trp 405	atc Ile	aag Lys	ccg Pro	ggc Gly	ggc Gly 410	gag Glu	1253
tgc Cys	gac Asp	ggc Gly	acc Thr 415	agc Ser	gac Asp	acc Thr	tcg Ser	gcc Ala 420	gcc Ala	cgc Arg	tac Tyr	gac Asp	cac His 425	ttc Phe	tgt Cys	1301
ggc Gly	aac Asn	cct Pro 430	gat Asp	gcc Ala	ctc Leu	aag Lys	ccg Pro 435	gcc Ala	ccc Pro	gaa Glu	gcc Ala	gga Gly 440	gag Glu	tgg Trp	ttc Phe	1349
cag	gcc	tac	ttc	gag	cag	ctt	ctg	cgc	aac	gcc	aac	ccc	gcc	ttc		1394

Sequence Listing CBH 10377-WO.ST25

Gln Ala Tyr Phe Glu Gln Leu Leu Arg Asn Ala Asn Pro Ala Phe
 445 450 455

taagtgtctg atgagctttt ctgagagggt acttccgcgg tcttgggttt cactcttctc 1454
 agcctttcag ggcagcagtt ttggtttctt ggggtaggac ctccgggttt atgtagacgg 1514
 agttaggaag ccaaactac tatgaatgta gtattcaaga agataatgac ttgaaaaaaaa 1574
 aaaaaaaaaa aaa 1587

<210> 24

<211> 458

<212> PRT

<213> Stibella annulata NP001040

<400> 24

Met Ala Gly Arg Phe Phe Leu Ser Ala Ala Phe Leu Ala Ser Ala Ala
 1 5 10 15

Leu Ala Val Pro Leu Glu Glu Arg Gln Asn Cys Ser Pro Gln Trp Ala
 20 25 30

Gln Cys Gly Gly Asn Gly Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly
 35 40 45

Ser Asn Cys Gln Val Thr Asn Glu Trp Tyr Ser Gln Cys Val Pro Gly
 50 55 60

Ala Ala Pro Pro Pro Pro Pro Val Thr Thr Thr Arg Ser Thr Thr Thr
 65 70 75 80

Pro Pro Thr Thr Thr Thr Arg Thr Thr Ala Asp Ala Pro Pro Pro Thr
 85 90 95

Gly Gly Ala Thr Tyr Thr Gly Asn Pro Phe Leu Gly Val Asn Gln Trp
 100 105 110

Ala Asn Asn Phe Tyr Arg Ser Glu Ile Met Asn Ile Ala Val Pro Ser
 115 120 125

Leu Ser Gly Ala Met Ala Thr Ala Ala Ala Lys Val Ala Asp Val Pro
 130 135 140

Thr Phe Gln Trp Ile Asp Lys Met Asp Lys Leu Pro Leu Ile Asp Glu
 145 150 155 160

Ala Leu Ala Asp Val Arg Ala Ala Asn Ala Arg Gly Gly Asn Tyr Ala
 165 170 175

Ser Ile Leu Val Val Tyr Asn Leu Pro Asp Arg Asp Cys Ala Ala Ala
 180 185 190

Ala Ser Asn Gly Glu Phe Ala Ile Ala Asp Gly Gly Val Ala Lys Tyr
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Sequence Listing CBH 10377-WO.ST25

195

200

205

Lys Asn Tyr Ile Asp Glu Ile Arg Lys Leu Val Ile Lys Tyr Asn Asp
 210 215 220

Leu Arg Ile Ile Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Met Val
 225 230 235 240

Thr Asn Met Asn Val Ala Lys Cys Gln Asn Ala Ala Ser Ala Tyr Arg
 245 250 255

Glu Cys Thr Asn Tyr Ala Leu Thr Asn Leu Asp Leu Pro Asn Val Ala
 260 265 270

Gln Tyr Met Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn
 275 280 285

Ile Thr Pro Ala Ala Gln Leu Phe Ala Glu Val Tyr Lys Gln Ala Gly
 290 295 300

Ser Pro Lys Ser Val Arg Gly Leu Ala Ile Asn Val Ser Asn Tyr Asn
 305 310 315 320

Ala Trp Ser Val Ser Ser Pro Pro Pro Tyr Thr Ser Pro Asn Pro Asn
 325 330 335

Tyr Asp Glu Arg His Phe Val Glu Ala Phe Ala Pro Leu Leu Arg Gln
 340 345 350

Asn Gly Trp Asp Ala Lys Phe Ile Val Asp Gln Gly Arg Ser Gly Arg
 355 360 365

Gln Pro Thr Gly Gln Gln Glu Trp Gly His Trp Cys Asn Ala Ile Gly
 370 375 380

Thr Gly Phe Gly Gln Arg Pro Thr Ser Asn Thr Gly His Ala Asp Val
 385 390 395 400

Asp Ala Phe Val Trp Ile Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser
 405 410 415

Asp Thr Ser Ala Ala Arg Tyr Asp His Phe Cys Gly Asn Pro Asp Ala
 420 425 430

Leu Lys Pro Ala Pro Glu Ala Gly Glu Trp Phe Gln Ala Tyr Phe Glu
 435 440 445

Gln Leu Leu Arg Asn Ala Asn Pro Ala Phe
 450 455

<210> 25

Sequence Listing CBH 10377-WO.ST25

<211> 1559
<212> DNA
<213> Malbrancheae cinnamonea NP001045

<220>
<221> CDS
<222> (41) .. (1210)

[illegible]

Sequence Listing CBH 10377-WO.ST25

215
 gag gtc tgg aat gca gct ggc agg cca aag tcc act cga ggg ttt gct 775
 Glu Val Trp Asn Ala Ala Gly Arg Pro Lys Ser Thr Arg Gly Phe Ala
 230 235 240 245

acg aac gtt tcc aac tac aac ggt tat tcc ctc agc acc gct cct ccc 823
 Thr Asn Val Ser Asn Tyr Asn Gly Tyr Ser Leu Ser Thr Ala Pro Pro
 250 255 260

tac act gag ccc aac ccc aat ttc gac gaa gtg cgt tat atc aat gca 871
 Tyr Thr Glu Pro Asn Pro Asn Phe Asp Glu Val Arg Tyr Ile Asn Ala
 265 270 275

ttc cgc cca ctc ctc gag gca cgg ggt ttc cca gca tac ttc atc gtc 919
 Phe Arg Pro Leu Leu Glu Ala Gln Gly Phe Pro Ala Tyr Phe Ile Val
 280 285 290

gac caa ggc cgc agc ggt gtc cag ccc act gcg cag att gag caa gga 967
 Asp Gln Gly Arg Ser Gly Val Gln Pro Thr Ala Gln Ile Glu Gln Gly
 295 300 305

cac tgg tgc aat gtg atc gac acc ggt ttt gga act cgc ccc act act 1015
 His Trp Cys Asn Val Ile Asp Thr Gly Phe Gly Thr Arg Pro Thr Thr
 310 315 320 325

gac act ggt aat gag tac gtt gac tcg atc gtg tgg gtg aag cct ggc 1063
 Asp Thr Gly Asn Glu Tyr Val Asp Ser Ile Val Trp Val Lys Pro Gly
 330 335 340

ggc gaa tcg gac gga acc agc gat acc tct gct gag aga tat gac tac 1111
 Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala Glu Arg Tyr Asp Tyr
 345 350 355

cac tgc gga ctt gag gat gca ttg aag cca gct cct gaa gcg gga cag 1159
 His Cys Gly Leu Glu Asp Ala Leu Lys Pro Ala Pro Glu Ala Gly Gln
 360 365 370

tgg ttc cag gcc tac ttc gag caa ctg ctc aga aat gcc aac ccc cca 1207
 Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu Arg Asn Ala Asn Pro Pro
 375 380 385

ttc taaatcagat gaaggacgga cccaattgat gacggcctgt cttcgtgac 1260
 Phe
 390

cgacgaaagc aatgtcaggg tgaaaatgac cgagagattg gagagtcattg aggataggta 1320

gtcaatgatt tcacccgagt ttccacgttt tacccttctt gtacatagtt tggagtcgcc 1380

tgttggtttc agtagtacat cttatccgac agagtctatc gtttgattac cccagtcaaa 1440

agcgttattg caatcttttc ctagggattt attgtttgct gcggatgtcg tggctatggg 1500

cagctgactg aattaaactg gaactcttgg tatccaaaaa aaaaaaaaaa aaaaaaaaaa 1559

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 <211> 390
 <212> PRT
 <213> Malbrancheae cinnamonea NP001045
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Sequence Listing CBH 10377-WO.ST25

Ser Ala Ser Pro Phe Leu Leu Pro Arg Gln Ala Asn Ser Ser Asn Pro
 20 25 30
 Phe Ala Gly His Thr Ile Tyr Pro Asn Pro Tyr Tyr Ser Asn Glu Ile
 35 40 45
 Asp Glu Phe Ala Ile Pro Ala Leu Gln Glu Thr Asp Pro Ala Leu Val
 50 55 60
 Glu Lys Ala Ala Leu Val Lys Glu Val Gly Thr Phe Phe Trp Ile Asp
 65 70 75 80
 Val Val Ala Lys Val Pro Asp Ile Gly Pro Tyr Leu Gln Gly Ile Gln
 85 90 95
 Glu Ala Asn Ala Ala Gly Gln Asn Pro Pro Tyr Ile Gly Ala Ile Val
 100 105 110
 Val Tyr Asp Leu Pro Asn Arg Asp Cys Ala Ala Ala Ala Ser Asn Gly
 115 120 125
 Glu Phe Ser Leu Glu Asp Gly Gly Glu Glu Lys Tyr Arg Gly Tyr Ile
 130 135 140
 Asp Gly Ile Arg Glu Gln Ile Glu Lys Tyr Pro Asp Val Arg Val Ala
 145 150 155 160
 Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Met Val Thr Asn Leu Asn
 165 170 175
 Val Pro Lys Cys Ala Glu Ser Glu Gln Ala Tyr Arg Asp Gly Val Ala
 180 185 190
 Tyr Ala Leu Lys Gln Leu Asp Leu Pro Asn Val Trp Thr Tyr Ile Asp
 195 200 205
 Ala Gly His Ser Gly Trp Leu Gly Trp Pro Ala Asn Ile Glu Pro Ala
 210 215 220
 Ala Glu Ile Phe Val Glu Val Trp Asn Ala Ala Gly Arg Pro Lys Ser
 225 230 235 240
 Thr Arg Gly Phe Ala Thr Asn Val Ser Asn Tyr Asn Gly Tyr Ser Leu
 245 250 255
 Ser Thr Ala Pro Pro Tyr Thr Glu Pro Asn Pro Asn Phe Asp Glu Val
 260 265 270
 Arg Tyr Ile Asn Ala Phe Arg Pro Leu Leu Glu Ala Arg Gly Phe Pro
 275 280 285

Sequence Listing CBH 10377-WO.ST25

Ala Tyr Phe Ile Val Asp Gln Gly Arg Ser Gly Val Gln Pro Thr Ala
 290 295 300

Gln Ile Glu Gln Gly His Trp Cys Asn Val Ile Asp Thr Gly Phe Gly
 305 310 315 320

Thr Arg Pro Thr Thr Asp Thr Gly Asn Glu Tyr Val Asp Ser Ile Val
 325 330 335

Trp Val Lys Pro Gly Gly Glu Ser Asp Gly Thr Ser Asp Thr Ser Ala
 340 345 350

Glu Arg Tyr Asp Tyr His Cys Gly Leu Glu Asp Ala Leu Lys Pro Ala
 355 360 365

Pro Glu Ala Gly Gln Trp Phe Gln Ala Tyr Phe Glu Gln Leu Leu Arg
 370 375 380

Asn Ala Asn Pro Pro Phe
 385 390

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 <211> 17
 <212> DNA
 <213> Artificial

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (1)..(17)
 <223> r is a or g

y is t or c

n is a, g, t, or c

<400> 27
 tggggncart gyggngg

17

<210> 28
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 <213> Artificial

<220>
 <223> Primer

<220>
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 <222> (1)..(17)
 <223> y is t or c

n is a, g, t, or c

<400> 28
 tggytnggnt ggccngc

17

Sequence Listing CBH 10377-WO.ST25

<210> 29
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer

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<222> (1)..(17)
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r is a or g

<400> 29
gcnggccanc cnarcca

17

<210> 30
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer

<220>
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<222> (1)..(17)
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n is a, g, t, or c

<400> 30
ttrcaccart cncccca

17

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<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer

<220>
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<222> (1)..(17)
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y is t or c

n is a, g, t or c

<400> 31
ggyttnaccc anacraa

17

<210> 32
<211> 17
<212> DNA
<213> Artificial

Sequence Listing CBH 10377-WO.ST25

<220>

<223> Primer

<220>

<221> misc_feature

<222> (1)..(17)

<223> r is a or g

y is t or c

n is a, g, t or c

<400> 32

aartangcyt graacca

17

<210> 33

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Primer

<220>

<221> misc_feature

<222> (1)..(25)

<400> 33

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25

<210> 34

<211> 34

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34

<210> 35

<211> 31

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 35

actggattta ccatggccgg tcgattcttc c

31

<210> 36

<211> 31

<212> DNA

<213> Artificial

Sequence Listing CBH 10377-WO.ST25

<220>

<223> Primer

<400> 36

agtcacctct agttattaga aggcgggggtt g

31